

CCAGCAGCTG	CAAGGTGCAA	GAAGAAGAAG	ATCCCAGGGA	GGAAAATGTG	50
CTGGAGACCC	CTGTGTCGG-	TTCCTGTGGC	TTTGGTCCTA	TCTGTCTTAT	100
GTTCAAGCAG	TGCCTATCCA	GAAAGTCCAG	GATGACACCA	AAACCCTCAT	150
CAAGACCATT	GTCACCAGGA	TCAATGACAT	TTCACACACG	CAGTCGGTAT	200
CCGCCAAGCA	GAGGGTCACT	GGCTTGGACT	TCATTCTCTG	GCTTCACCCC	250
ATTCTGAGTT	GTTCCAAGAT	GGACCAGACT	CTGGCAGTCT	ATCAACAGGT	300
CCTCACCAGC	CTGCCTTCCC	AAAATGTGCT	GCAGATAGCC	AATGACCTGG	350
AGAATCTCCG	AGACCTCCTC	CATCTGCTGG	CCTTCTCCAA	GAGCTGCTCC	400
CTGCCTCAGA	CCAGTGGCCT	GCAGAAGCCA	GAGAGCCTGG	ATGGCGTCCT	450
GGAAGCCTCA	CTCTACTCCA	CAGAGGTGGT	GGCTTTGAGC	AGGCTGCAGG	500
GCTCTCTGCA	GGACATTCTT	CAACAGTTGG	ATGTTAGCCC	TGAATGCTGA	550
AGTTTCAAAG	GCCAC-CAGG	CTCCCAAGAA	TCATGTAGAG	GGAAGAAACC	600
TTGGCTTCCA	GGGGTCTTCA	GGA--GAAGA	G-AGC-CATG	TGCACAC---	650
ATCCA-----T	CATTCA-TTT	CTCTCCCTCC	TGTAGACCAC	-----CCAT--	700
-					701

FIG. 1

---G--GTTG	CAAGGCCCAA	GAAGCCCA--	-TCCTGGGAA	GGAAAATGCA	50
TTGGGGAACC	CTGTG-CGGA	TTCTTGTGGC	TTTGGCCCTA	TCTTTTCTAT	100
GTCCAAGCTG	TGCCCATCCA	AAAAGTCCAA	GATGACACCA	AAACCCTCAT	150
CAAGACAATT	GTCACCAGGA	TCAATGACAT	TTCACACACG	CAGTCAGTCT	200
CCTCCAAACA	GAAAGTCACC	GGTTTGGACT	TCATTCCCTGG	GCTCCACCCC	250
ATCCTGACCT	TATCCAAGAT	GGACCAGACA	CTGGCAGTCT	ACCAACAGAT	300
CCTCACCAGT	ATGCCTTCCA	GAAACGTGAT	CCAAATATCC	AACGACCTGG	350
AGAACCTCCG	GGATCTTCTT	CACGTGCTGG	CCTTCTCTAA	GAGCTGCCAC	400
TTGCCCTGGG	CCAGTGGCCT	GGAGACCTTG	GACAGCCTGG	GGGGTGTCTT	450
GGAAGCTTCA	GGCTACTCCA	CAGAGGTGGT	GGCCCTGAGC	AGGCTGCAGG	500
GGTCTCTGCA	GGACATGCTG	TGGCAGCTGG	ACCTCAGCCC	TGGGTGCTGA	550
GGCCTTGAAG	GTCACTCTTC	CTGCAAGGAC	T-ACGTTAAG	GGAAGGAACT	600
CTGGTTTCCA	GGTATCTCCA	GGATTGAAGA	GCATTGCATG	GACACCCCTT	650
ATCCAGGACT	CTGTCAATTT	CCCTGACTCC	TCTAAGCCAC	TCTTCCAAAG	700
G					701

FIG. 2

1	Met Cys Trp Arg Pro Leu Cys Arg Phe Leu Trp Leu Trp Ser Tyr
16	Leu Ser Tyr Val Gln Ala Val Pro Ile Gln Lys Val Gln Asp Asp
31	Thr Lys Thr Leu Ile Lys Thr Thr Ile Val Thr Arg Ile Asn Asp Ile
46	Ser His Thr Gln Ser Val Ser Ala Lys Gln Arg Val Thr Gly Leu
61	Asp Phe Ile Pro Gly Leu His Pro Ile Leu Ser Leu Ser Lys Met
76	Asp Gln Thr Leu Ala Val Tyr Gln Gln Val Leu Thr Ser Leu Pro
91	Ser Gln Asn Val Leu Gln Ile Ala Asn Asp Leu Glu Asn Leu Arg
106	Asp Leu Leu His Leu Leu Ala Phe Ser Lys Ser Cys Ser Leu Pro
121	Gln Thr Ser Gly Leu Gln Lys Pro Glu Ser Leu Asp Gly Val Leu
136	Glu Ala Ser Leu Tyr Ser Thr Glu Val Val Ala Leu Ser Arg Leu
151	Gln Gly Ser Leu Gln Asp Ile Leu Gln Gln Leu Asp Val Ser Pro
166	Glu Cys End

FIG.3

1 MET HIS TRP GLY THR LEU CYS GLY PHE LEU TRP LEU TRP PRO TYR
16 LEU PHE TYR VAL GLN ALA VAL PRO ILE GLN LYS VAL GLN ASP ASP
31 THR LYS THR LEU ILE LYS THR ILE VAL THR ARG ILE ASN ASP ILE
46 SER HIS THR GLN SER VAL SER SER LYS GLN LYS VAL THR GLY LEU
61 ASP PHE ILE PRO GLY LEU HIS PRO ILE LEU THR LEU SER LYS MET
76 ASP GLN THR LEU ALA VAL TYR GLN GLN ILE LEU THR SER MET PRO
91 SER ARG ASN VAL ILE GLN ILE SER ASN ASP LEU GLU ASN LEU ARG
106 ASP LEU LEU HIS VAL LEU ALA PHE SER LYS SER CYS HIS LEU PRO
121 TRP ALA SER GLY LEU GLU THR LEU ASP SER LEU GLY GLY VAL LEU
136 GLU ALA SER GLY TYR SER THR GLU VAL VAL ALA LEU SER ARG LEU
151 GLN GLY SER LEU GLN ASP MET LEU TRP GLN LEU ASP LEU SER PRO
166 GLY CYS END

FIG.4

1	MET	CYS	TRP	ARG	PRO	LEU	CYS	ARG	PHE	LEU	TRP	LEU	TRP	SER	TYR
16	LEU	SER	TYR	VAL	GLN	ALA	VAL	PRO	ILE	GLN	LYS	VAL	GLN	ASP	ASP
31	THR	LYS	THR	LEU	ILE	LYS	THR	ILE	VAL	THR	ARG	ILE	ASN	ASP	ILE
46	SER	HIS	THR	SER	VAL	SER	ALA	LYS	GLN	ARG	VAL	THR	GLY	LEU	ASP
61	PHE	ILE	PRO	GLY	LEU	HIS	PRO	ILE	LEU	SER	LEU	SER	LYS	MET	ASP
76	GLN	THR	LEU	ALA	VAL	TYR	GLN	GLN	VAL	LEU	THR	SER	LEU	PRO	SER
91	GLN	ASN	VAL	LEU	GLN	ILE	ALA	ASN	ASP	LEU	GLU	ASN	LEU	ARG	ASP
106	LEU	LEU	HIS	LEU	LEU	ALA	PHE	SER	LYS	SER	CYS	SER	LEU	PRO	GLN
121	THR	SER	GLY	LEU	GLN	LYS	PRO	GLU	SER	LEU	ASP	GLY	VAL	LEU	GLU
136	ALA	SER	LEU	TYR	SER	THR	GLU	VAL	VAL	ALA	LEU	SER	ARG	LEU	GLN
151	GLY	SER	LEU	GLN	ASP	ILE	LEU	GLN	GLN	LEU	ASP	VAL	SER	PRO	GLU
166	CYS END														

FIG.5

1	MET	HIS	TRP	GLY	THR	LEU	CYS	GLY	PHE	LEU	TRP	LEU	TRP	PRO	TYR
16	LEU	PHE	TYR	VAL	GLN	ALA	VAL	PRO	ILE	GLN	LYS	VAL	GLN	ASP	ASP
31	THR	LYS	THR	LEU	ILE	LYS	THR	ILE	VAL	THR	ARG	ILE	ASN	ASP	ILE
46	SER	HIS	THR	SER	VAL	SER	SER	LYS	GLN	LYS	VAL	THR	GLY	LEU	ASP
61	PHE	ILE	PRO	GLY	LEU	HIS	PRO	ILE	LEU	THR	LEU	SER	LYS	MET	ASP
76	GLN	THR	LEU	ALA	VAL	TYR	GLN	GLN	ILE	LEU	THR	SER	MET	PRO	SER
91	ARG	ASN	VAL	ILE	GLN	ILE	SER	ASN	ASP	LEU	GLU	ASN	LEU	ARG	ASP
106	LEU	LEU	HIS	VAL	LEU	ALA	PHE	SER	LYS	SER	CYS	HIS	LEU	PRO	TRP
121	ALA	SER	GLY	LEU	GLU	THR	LEU	ASP	SER	LEU	GLY	GLY	VAL	LEU	GLU
136	ALA	SER	GLY	TYR	SER	THR	GLU	VAL	VAL	ALA	LEU	SER	ARG	LEU	GLN
151	GLY	SER	LEU	GLN	ASP	MET	LEU	TRP	GLN	LEU	ASP	LEU	SER	PRO	GLY
166	CYS	END													

FIG.6

FIG. 7

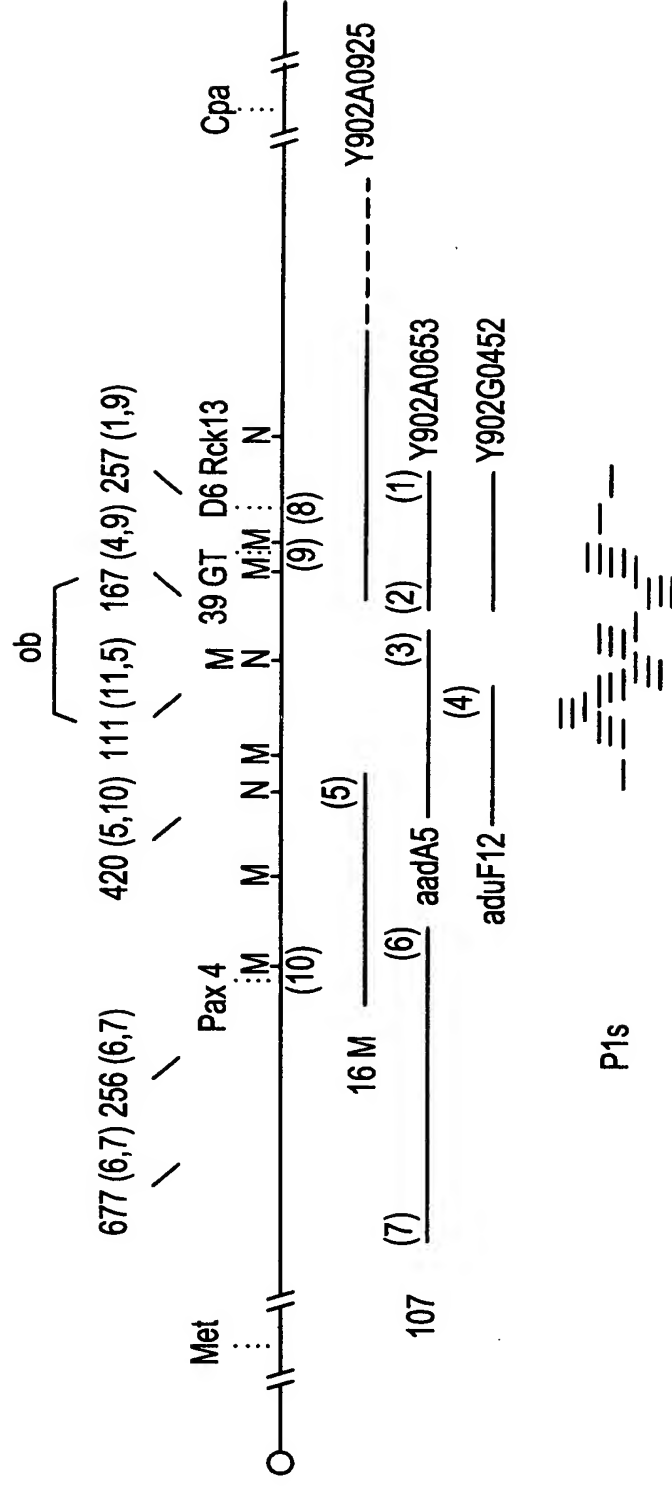


FIG. 8

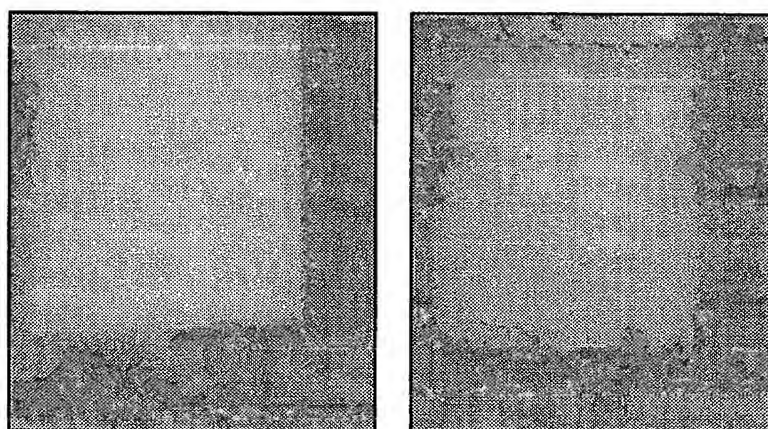
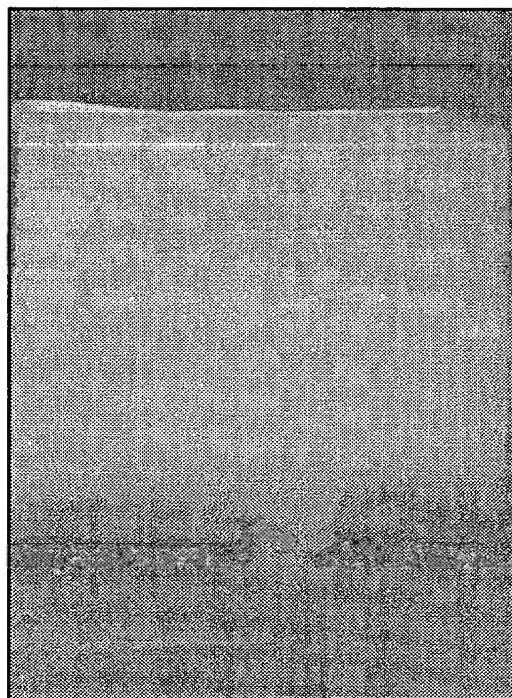


FIG. 9

1 2 3 4 5 6 7



+10	+20	+30	+40
GTGCAAGAAG	AAGAAGATCC	CAGGGCAGGA	AAATGTGCTG
-----	-----	-----	-----
CAGGTTCTTC	TTCTTCTAGG	GTCCCGTCCT	TTTACACGAC
-----	-----	-----	-----
+10	+20	+30	+40
TGTCGGGTCC	NGTGGNTTTG	GTCCATCTCG	TCTTAAGTNC
-----	-----	-----	-----
ACAGCCCAGG	NCACCNAAAC	CAGGATAGAC	AGAATACANG
-----	-----	-----	-----
+10	+20	+30	+40
TATCCAGAAA	GTCCAGGATG	ACACCAAAG	CCTCATCAAG
-----	-----	-----	-----
ATAGGTCCTT	CAGGTCCTAC	TGTGGTTTTC	GGAGTAGTTC
-----	-----	-----	-----
+10	+20	+30	+40
NCAGGATCAC	TGANATTICA	CACACG	
-----	-----	-----	-----
NGTCCTAGTG	ACTNTAAAGT	GTGTGC	

FIG.10

FIG. 11

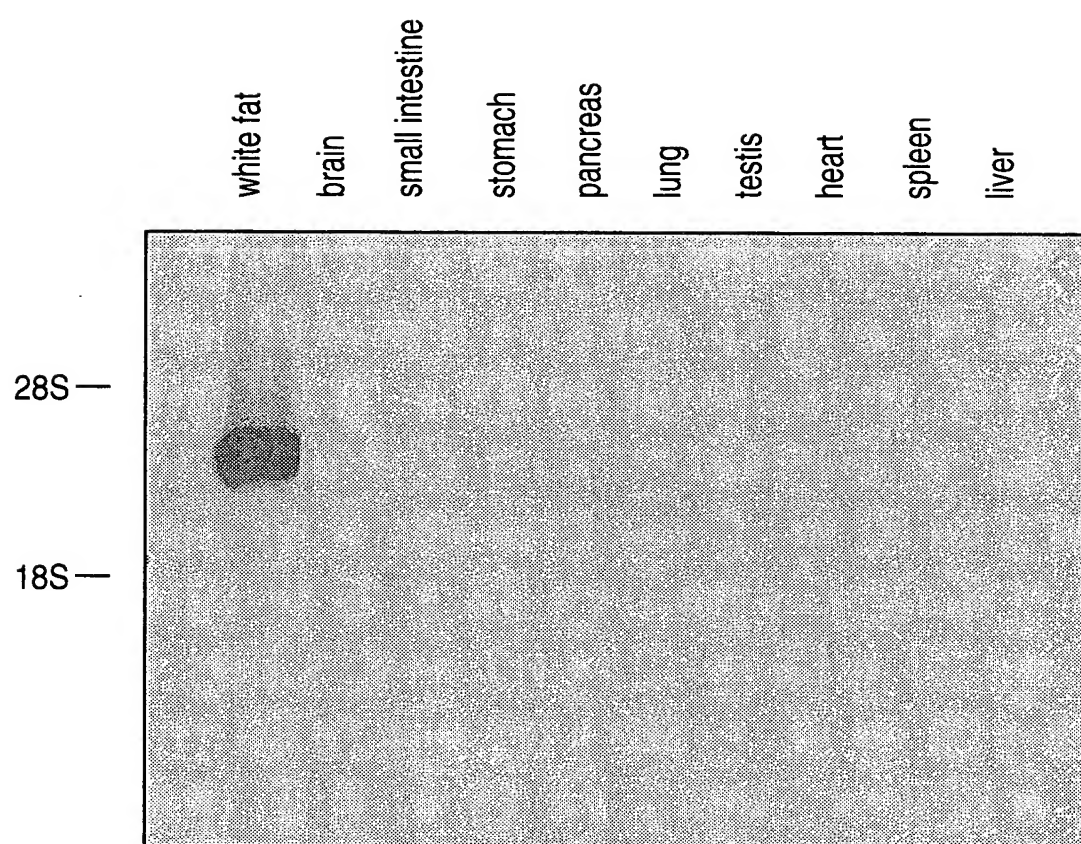


FIG. 12

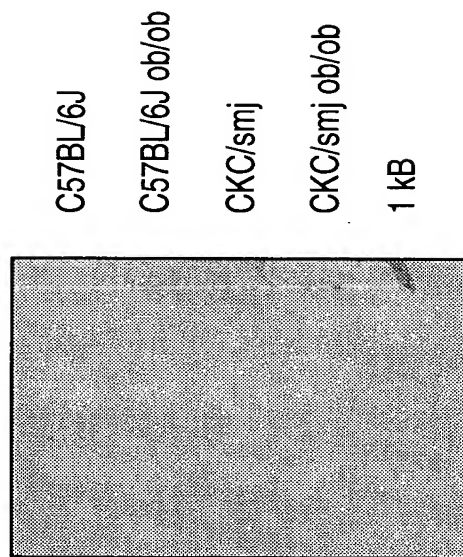


FIG. 13

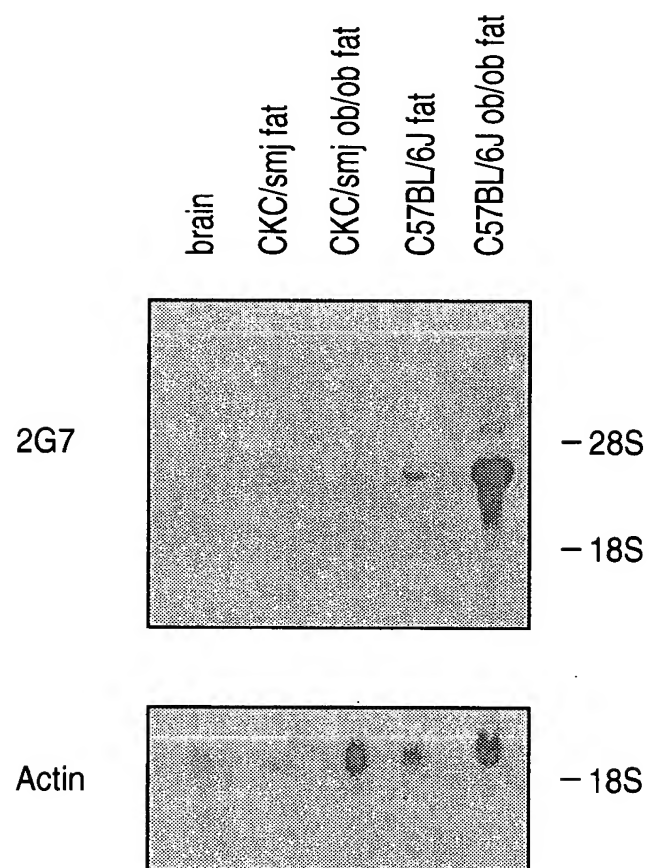
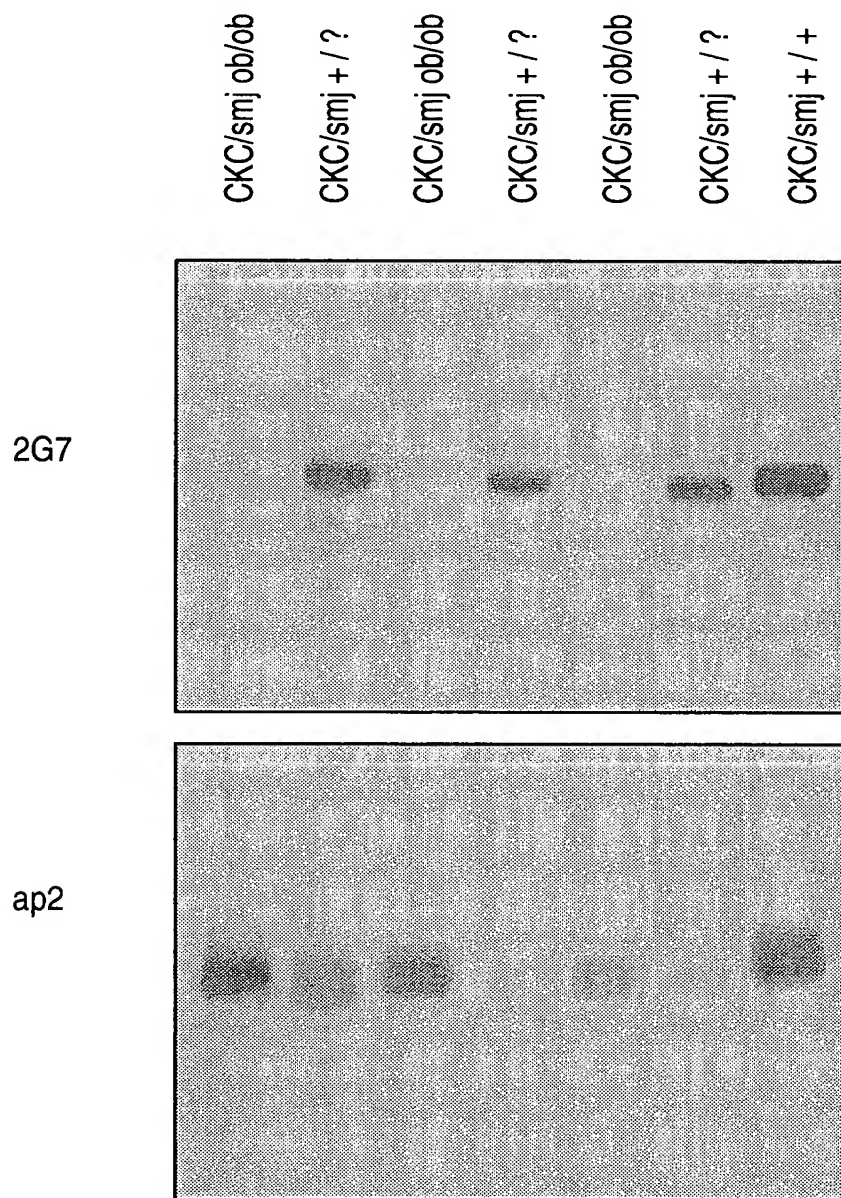


FIG. 14



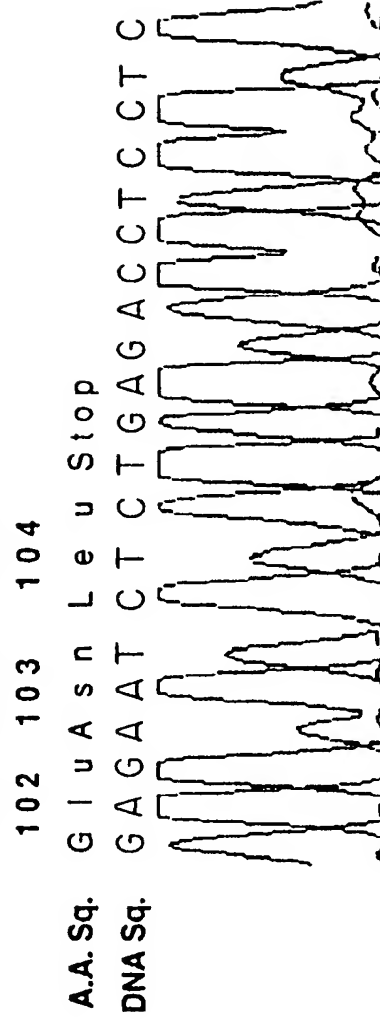
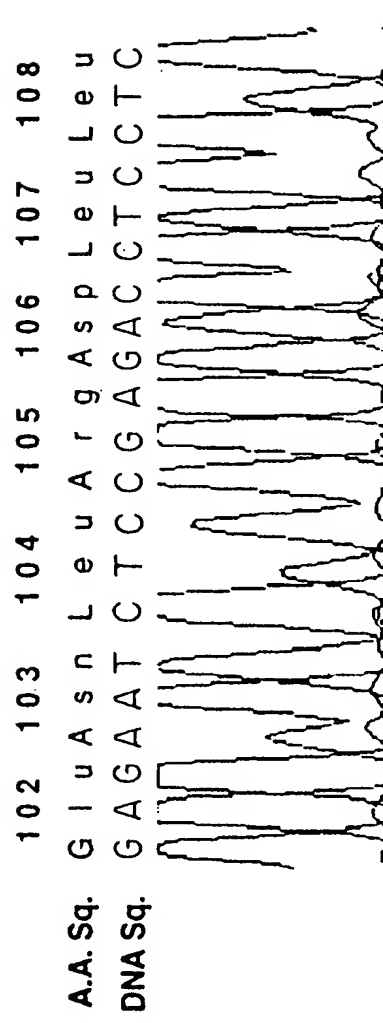


FIG.15

FIG. 16

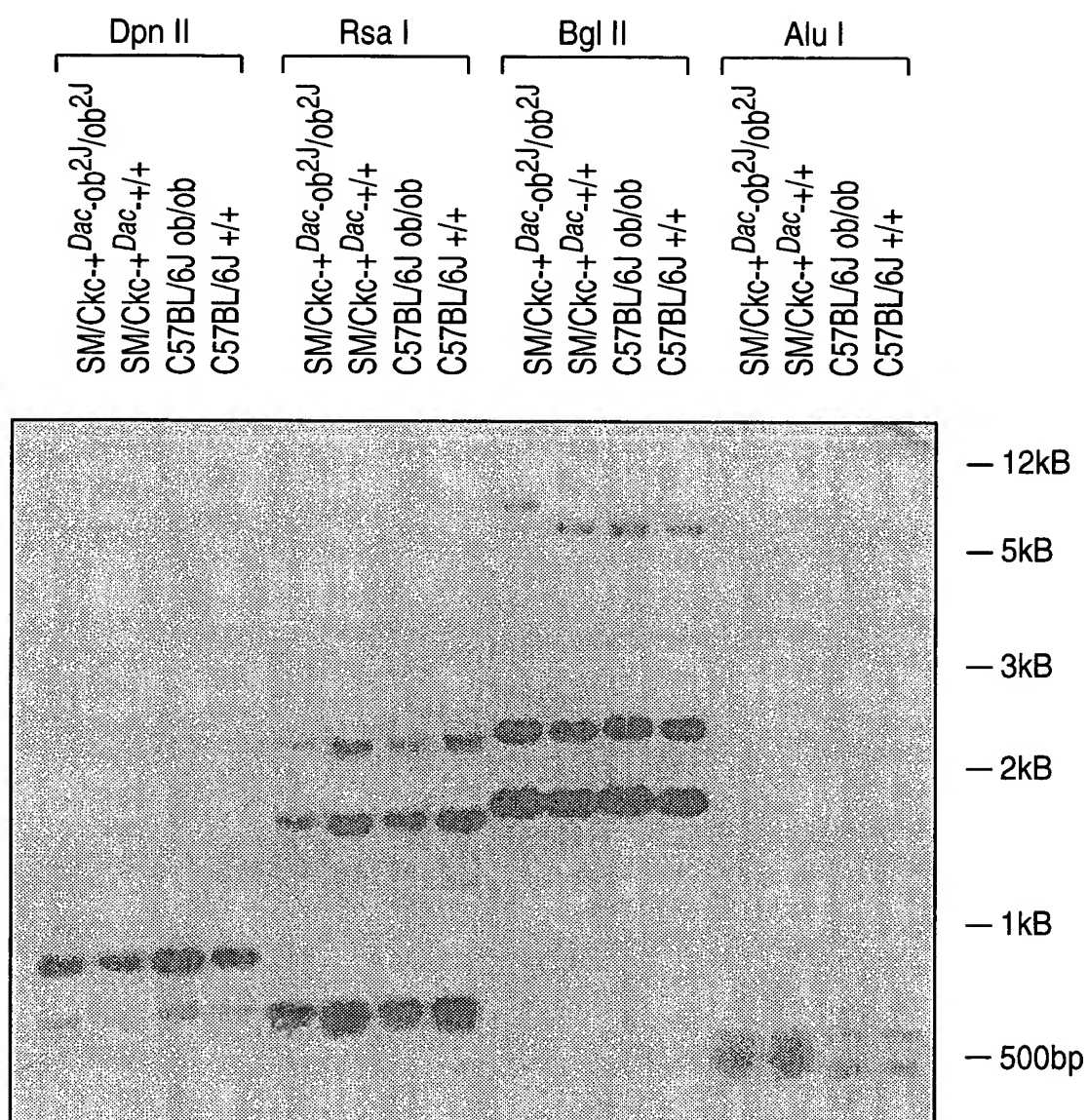


FIG. 17

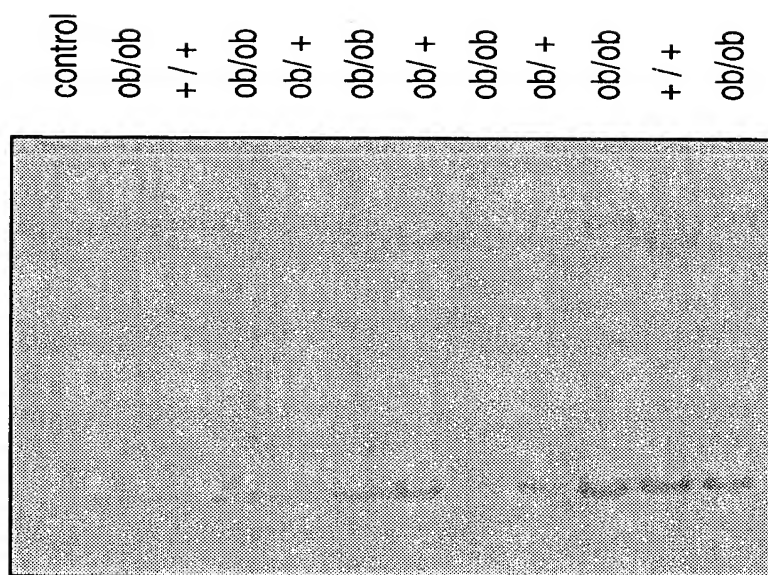
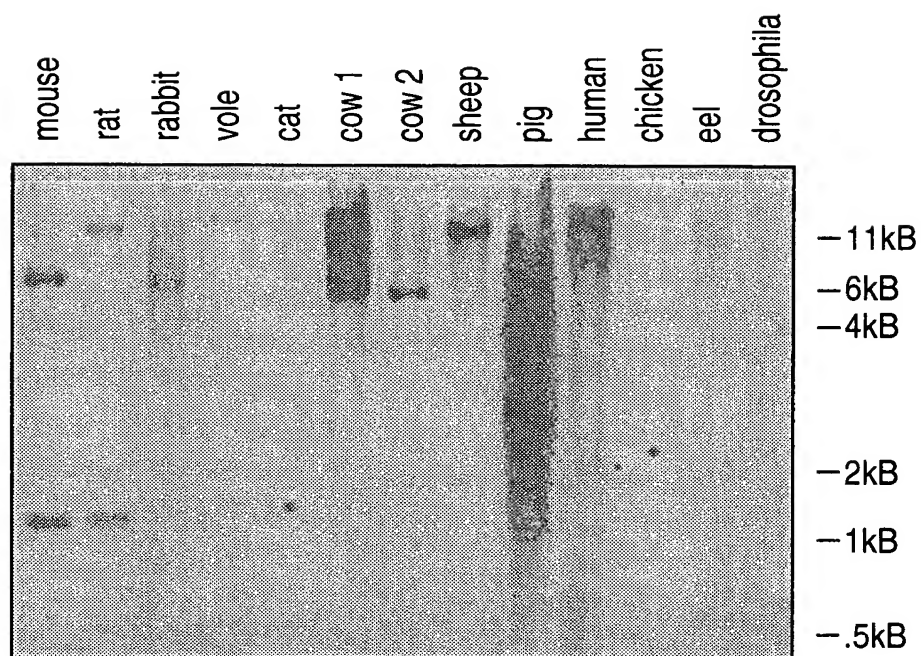


FIG. 18



T7 PROMOTER PRIMER 69348-1

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T7 PROMOTER

BGLII AGATCTCGATCCCGGAAATTAATACGACTCACTATAGGGAAATTGTGAGCGGATAACAATTCCCCTCTACA LAC OPERATOR XBAI

RBS NcoI HIS-TAG
AATAATTTTGTTTAACTTTAAGAGGAGATATACCATGGGCAGCAGCCATCATCATCATCAGCAGCGGC
METGLYSERSEHISHISHISHISERSERGLY

NDEI XhoI BamHI

CTGGTCCGCGGCAGCCATATGCTCGAGGATCCCGTGCTAACAAAGCCGAAAGGAGCTGAGTTGGCT
LEUVALPROARGGLYSERHISMETLEUGLUASPPROALAAASNLYSALAARGLYSGLUALAGLULEUALA
THROMBIN

BpuI1021

GCTGCCACCGCTGAGCAATAAGCATAACCCCTTGGGGCCTCTAAACGGGTCTTGAGGGGTTTTTG
ALAAALATHRALAGLUGLNEND

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T7 TERMINATOR PRIMER #69337-1

FIG.19